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1646

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FEB 20 2001

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/380,276A

DATE: 02/16/2001

TIME: 10:24:01

Input Set : N:\i380276.raw

Output Set: N:\CRF3\02162001\I380276A.raw

C--> 1 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.  
 2 <120> TITLE OF INVENTION: Novel Polypeptides, DNAs encoding the polypeptides, and utility of the  
 3 Polypeptides  
 4 <130> FILE REFERENCE: Q55589  
 5 <140> CURRENT APPLICATION NUMBER: US/09/380,276A  
 6 <141> CURRENT FILING DATE: 1997-02-27  
 7 <150> PRIOR APPLICATION NUMBER: JP 9-43143  
 8 <151> PRIOR FILING DATE: 1997-02-27  
 9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00799  
 10 <151> PRIOR FILING DATE: 1997-02-27  
 11 <160> NUMBER OF SEQ ID NOS: 10  
 12 <170> SOFTWARE: PatentIn version 3.0  
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 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Homo sapiens  
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 21 gatcgtcttg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag 180  
 22 gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacagggttc 240  
 23 aaggaggact ggggcttcca gaaatgcaag cctgtgtctgg actgcgcagt ggtgaaccgc 300  
 24 ttccagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga 360  
 25 ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac 420  
 26 cctcctcttc cttacgaacc gcaactgtgcc agcaagggtca acctcgtgaa gatcgcgtcc 480  
 27 acggcctcca gccacgggga cagggcgctg gctgccgtta tctgcagcgc tctggccacc 540  
 28 gtcctgctgg cctgtctcat cctctgtgtc atctattgta agagacagtt tatggagaag 600  
 29 aaaccagcgt ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt 660  
 30 cttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac 720  
 31 tcagtgcaga cctgcggggc ggtgcgcttg ctcccatcca tgtgctgtga ggaggcctgc 780  
 32 agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga 840  
 33 aacgcaggcc cagccgggga gatggtgccg actttcttcg gatccctcac gcagtccatc 900  
 34 tgtggcgagt ttccagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc 960  
 35 tctttttgtg actcttatcc tgaactcaact ggagaagaca ttattctctt caatccagaa 1020  
 36 cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctggt 1080  
 37 ccagtccagt ctcattctga aaactttaca gcagctactg atttatctag atataacaac 1140  
 38 aactggtag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag 1200  
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see p 5

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52      tccagaaatg caagccctgt ctggactgcg cagtgggtgaa ccgctttcag aaggcaaatt 360
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54      aacttgctcg ctttcaagac atggagtgtg tgccttgagg agaccctcct cctccttaag 480
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56      gggacacggc gctgggtgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc 600
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62      gggagatggt gccgactttc ttcggtatcc tcacgcagtc catctgtggc gaggtttcag 960
63      atgcctggcc tctgatgcag aatcccatgg gtggtgacaa catctctttt tgtgactctt 1020
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67      catcaactca ggatgcacta actatgagaa gccagctaga tcaggagagt ggcgctatca 1260
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69      agaagcgtgt gctggaaccc aaagagtact cctttgttag gcttatggac tgagcagctc 1380
70      ggaccttgca tggcttcttg ggcaaaaata aatctgaacc aaactgacgg catttgaaag 1440
71      ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa 1500
72      gaaaagactc caggccgact catgatactc tgcattcttc ctacatgaga agcttctctg 1560
73      ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat 1620
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79 <212> TYPE: DNA
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82 <221> NAME/KEY: misc_feature
83 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
84 <221> NAME/KEY: CDS
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86 <221> NAME/KEY: sig_peptide
87 <222> LOCATION: (45)..(119)
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93                                     -25
94      gtg cta cta gaa caa gag aaa acg ttt ttc act ctt tta gta tta cta 104
95      Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu Leu Val Leu Leu
96      -20 -15 -10
97      ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga gac tgt aga cag 152
98      Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly Asp Cys Arg Gln
99      -5 -1 1 5 10

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100	caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc tgc aac cag tgt	200
101	Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro Cys Asn Gln Cys	
102	15 20 25	
103	ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc ggc tat ggg gag	248
104	Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu	
105	30 35 40	
106	gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc aag gag gac tgg	296
107	Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe Lys Glu Asp Trp	
108	45 50 55	
109	ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca gtg gtg aac cgc	344
110	Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala Val Val Asn Arg	
111	60 65 70 75	
112	ttt cag aag gca aat tgt tca gcc acc agt gat gcc atc tgc ggg gac	392
113	Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala Ile Cys Gly Asp	
114	80 85 90	
115	tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc ggc ttt caa gac	440
116	Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp	
117	95 100 105	
118	atg gag tgt gtg cct tgt gga gac cct cct cct cct tac gaa ccg cac	488
119	Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His	
120	110 115 120	
121	tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc acg gcc tcc agc	536
122	Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser Thr Ala Ser Ser	
123	125 130 135	
124	cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc gct ctg gcc acc	584
125	Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr	
126	140 145 150 155	
127	gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat tgt aag aga cag	632
128	Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg Gln	
129	160 165 170	
130	ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca cag gac att cag	680
131	Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser Gln Asp Ile Gln	
132	175 180 185	
133	tac aac ggc tct gag ctg tgc tgt ctt gac aga cct cag ctc cac gaa	728
134	Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro Gln Leu His Glu	
135	190 195 200	
136	tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac tca gtg cag acc	776
137	Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp Ser Val Gln Thr	
138	205 210 215	
139	tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt gag gag gcc tgc	824
140	Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys Glu Glu Ala Cys	
141	220 225 230 235	
142	agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat tct gca gcc agt	872
143	Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser	
144	240 245 250	
145	ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc	920
146	Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe	
147	255 260 265	
148	ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg	968

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152   Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp
153           285           290           295
154   tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa   1064
155   Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu
156   300           305           310           315
157   ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt   1112
158   Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val
159           320           325           330
160   ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct   1160
161   Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala
162           335           340           345
163   act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act   1208
164   Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr
165           350           355           360
166   cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct   1256
167   Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala
168           365           370           375
169   atc atc cac cca gcc act cag acg tcc ctc cag gaa gct taaagaacct   1305
170   Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu Ala
171   380           385           390
172   gcttcttttct gcagtagaag cgtgtgctgg aacccaaaga gtactccttt gttaggctta   1365
173   tggactgagc agtctggacc ttgcatggct tctggggcaa aaataaatct gaaccaaact   1425
174   gacggcattt gaagcctttc agccagttgc ttctgagcca gaccagctgt aagctgaaac   1485
175   ctcaatgaat aacaagaaaa gactccaggc cgactcatga tactctgcat ctttcttaca   1545
176   tgagaagctt ctctgccaca aaagtgactt caaagacgga tgggttgagc tggcagccta   1605
177   tgagattgtg gacatataac aagaaacaga aatgccctca tgcttatttt catggtgatt   1665
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186 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
187 <400> SEQUENCE: 4
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192   Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
193           10           15           20
194   Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
195           25           30           35
196   Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
197           40           45           50           55
198   Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala

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203		90		95		100
204	Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro					
205		105		110		115
206	Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser					
207	120		125		130	135
208	Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser					
209		140		145		150
210	Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr					
211		155		160		165
212	Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser					
213		170		175		180
214	Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro					
215		185		190		195
216	Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp					
217	200		205		210	215
218	Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys					
219		220		225		230
220	Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His					
221		235		240		245
222	Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met					
223		250		255		260
224	Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe					
225		265		270		275
226	Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile					
227	280		285		290	295
228	Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser					
229		300		305		310
230	Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser					
231		315		320		325
232	Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn					
233		330		335		340
234	Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu					
235		345		350		355
236	Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln					
237	360		365		370	375
238	Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu					
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248	ggctatttgt catgtaaagt gacttgtgaa acaggagact gtagacagca agaattcagg				120	

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY                      DATE: 02/16/2001  
PATENT APPLICATION: US/09/380,276A        TIME: 10:24:02

Input Set : N:\i380276.raw  
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L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:474 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:474 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9